AMENDMENTS TO THE SPECIFICATION:

Please replace the paragraph beginning on page 2, line 12 (which was previously amended in the amendments dated August 9, 2000, and July 20, 2001), with the following rewritten paragraph:

--Figures 6A-6E show the complete nucleotide sequence of the *fig* gene from *S. epidermidis* strain HB and the deduced amino acid sequence of the encoded protein (SEQ ID NO:14). A putative ribosomal binding site (RBS) is underlined and a possible transcription termination hairpin loop is double underlined. A putative signal sequence (S) is indicated with an arrow and the translational stop codon with an asterix. The start of the non-repetitive N-terminal region called A, harbouring the fibrinogen binding activity is indicated by an arrow. R indicates the highly repetitive region. The 5 amino acid motif ~~LPXTG~~ involved in cell wall anchoring is indicated in bold characters and the membrane-spanning region is marked M (Example 3 ).--

J1

Please replace the paragraph beginning on page 10, line 6 (which was previously amended in the amendments dated August 9, 2000, and July 20, 2001), with the following rewritten paragraph:

--To obtain the missing 5' and 3' end of the *fig* gene a Southern blot analysis was performed using chromosomal DNA from strain HB digested with various restriction enzymes. The probe was prepared as follows; two oligonucleotides (5'CAACAACCATCTCACACAAC3' which is SEQ ID NO:1 and 5'CATCAAATTGATATTTCCCATC3' which is SEQ ID NO:2) were used to PCR amplify a ~1.3kb fragment from the insert of pSE100. The PCR generated

J2

fragments were 32P-labeled using random priming. After hybridisation using stringent conditions the NC-filter was washed and subjected to autoradiography. The result showed that the XbaI cleavage gave a single band in size of ~6 kb. The corresponding fragment was subsequently ligated into XbaI digested pUC18 vector. After transformation clones harbouring the ~6kb XbaI-fragment were identified by colony hvbridisation using the same probe as in the Southern blot experiment. One such clone, called pSE101 was chosen for further studies. DNA sequence analysis showed that the fig gene consist of an open reading frame of a 3291 nt, encoding a protein, called FIG of 1097 aa with a calculated molecular mass of ~119 kDa (figures 6A-6E). The FIG protein consist of several typical features found among Gram-positive cell surface bound proteins, like a N-terminal signal sequence and a C-terminal 5 amino acid ~~aa~~ motif ~~LPDTG~~, followed by a stretch of 17 hydrophobic aa ending in a stretch of charged aa (Figure 6). Following the signal sequence, there is a region, called A of 773 aa. The insert of pSE100 contains the sequence corresponding to residue 75 to 656 of the A region (Figure. 7). The A region is followed by a highly repetitive region of 216 aa composed of tandemly repeated aspartic acid and secine residues, called R (figures 6A-6E and 7). The dipeptid region consist of an 18 bp sequence unit (consensus of GAX TCX GAX TCX GAX AGX which is SEQ ID NO:3) repeated 36 times. The 18 bp sequence is almost maintained perfect throughout the whole R region except for the second unit which is truncated, consisting of only 12 of the 18 bp and the 3' end of the region where the consensus sequence is slightly disrupted (units 32, 34 and 36). The changes in the later units also result in an amino acid exchange which disrupt the DS repeat.